

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Kun On: October 5, 2002, 03:30:35 ; Search time 1713.89 Seconds  
(without alignments)  
3709.145 Million cell updates/sec

Title: US-09-525-361A-23  
Perfect score: 471  
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Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: em\_estro:\*  
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9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	403.2	85.6	432	10 W72838	W72838 zd57g12.s1
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4	388.6	82.5	423	10 BF742809	BF742809 IL2-BT080
5	379	80.5	402	9 A1139456	A1139456 qc20g01.x
6	345.2	73.3	454	10 BG202312	BG202312 RST21668
7	331	70.3	376	10 BG218084	BG218084 RST37810
8	316.8	67.3	345	9 BE092421	BE092421 CM1-BT073
9	309.8	65.8	391	10 BG185269	BG185269 RST4208 A
10	308.8	65.6	403	10 BG185269	R75793 y121f09.r1
11	301.4	64.0	314	12 A2694036	A2694036 AST-2H8BG
12	299.2	63.5	343	10 BG202313	BG202313 RST21669
13	294	62.4	313	9 AW176044	AW176044 QV0-BT010
14	289.4	61.4	294	9 AA340069	AA340069 EST45219
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16	281	59.7	316	10 BE926938	BE926938 CM1-BT073
17	255.8	54.3	443	9 A1127172	A1127172 qb99a08.x

18	247.6	52.6	308	9 A1905687	A1905687 IL-R-BT095-
19	217.8	46.2	251	10 BG197186	BG197186 RST16A24
20	202.8	43.1	221	9 BE074512	BE074512 IL5-BT057
21	197.8	42.0	462	9 AW294149	AW294149 UI-H-BT2-
22	197	41.8	224	9 AW291950	AW291950 UI-H-BT2-
23	196.6	41.7	230	10 BE815819	BE815819 PM3-BN017
24	187.8	39.9	248	10 BE815824	BE815824 PM3-BN017
25	159	33.8	193	9 A1905624	A1905624 CM-BT094-
26	154	32.7	224	9 A1905837	A1905837 IL-BT099-
27	151	32.1	211	10 BG183176	BG183176 RST2047 A
28	150	31.8	212	10 BG192597	BG192597 RST11712
29	149.4	29.8	178	9 A1905623	A1905623 CM-BT094-
30	140.4	29.7	211	10 BG207535	BG207535 RST27017
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37	82.4	17.5	492	10 B1279431	B1279431 UI-R-DA0-
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44	80.8	17.2	495	10 B1279214	B1279214 UI-R-DA0-
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ALIGNMENTS

RESULT 1

LOCUS W72837

DEFINITION zd57g12.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone, 5' element, similar to contains element MER40 repetitive element, mRNA sequence.

ACCESSION W72837

VERSION W72837.1

KEYWORDS GI:1382813

SOURCE EST.

ORGANISM human.

REFERENCE 1 (bases 1 to 436)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LLNL: contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 508 Std Error: 0.00

Seq primer: mob.REGA+ET.

Location/Qualifiers

1. 436

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/db\_xref="GDB:1270181"

/db\_xref="taxon:9606"

/clone="IMAGE:344806"

/dev\_stage="unknown"

/lab\_host="DH10B (ampicillin resistant)"





















GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 03:59:20 ; Search time 46.3 Seconds  
(without alignments)  
2498.777 Million cell updates/sec

Title: US-09-525-361A-23  
Perfect score: 471  
Sequence: 1 ctttgaagcattttgtctg.....aactatgagcagctaacat 471

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	68.6	14.6	397	3	US-09-253-691-3
3	65.4	13.9	477	4	US-09-135-994-1
4	65	13.8	234	1	US-08-469-802B-3
5	65	13.8	234	2	US-08-267-803B-3
6	64.8	13.8	3376	1	US-08-320-559-29
7	64.8	13.8	3376	3	US-08-545-860D-29
8	64.8	13.8	3376	5	PCT-US94-04496-29
9	64.6	13.7	203	4	US-09-043-303-7
10	63.4	13.5	168	1	US-08-469-802B-4
11	63.4	13.5	168	2	US-08-267-803B-4
12	63.4	13.5	171	1	US-08-469-802B-5
13	63.4	13.5	171	2	US-08-267-803B-5
14	63.4	13.5	195	1	US-08-469-802B-2
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19	52.6	11.2	2580	3	US-09-050-863-2
20	52.6	11.2	2580	4	US-09-359-081-2
21	52.6	11.2	3489	2	US-08-728-323A-1
22	52.6	11.2	5452	2	US-09-130-114-1
23	52.6	11.2	9600	4	US-08-910-647-1
24	52.6	11.2	10596	1	US-07-884-811-15
25	52.6	11.2	10596	1	US-07-885-971-15
26	52.6	11.2	10596	1	US-08-087-763A-15
27	52.6	11.2	10596	1	US-08-194-088B-15

C 28	52.6	11.2	10596	2	US-08-194-087-15	Sequence 15, Appl
C 29	52.6	11.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl
C 30	52.6	11.2	32207	2	US-08-770-379-20	Sequence 20, Appl
C 31	52.6	11.2	32207	4	US-08-757-669A-20	Sequence 20, Appl
C 32	52.6	11.2	32207	4	US-09-230-371A-20	Sequence 20, Appl
C 33	52	11.0	2790	2	US-08-718-661-1	Sequence 1, Appl
C 34	51.2	10.9	1518	2	US-08-820-170A-20	Sequence 20, Appl
C 35	51.2	10.9	1518	3	US-09-055-699-20	Sequence 20, Appl
C 36	51.2	10.9	1518	4	US-09-273-565-20	Sequence 20, Appl
C 37	51.2	10.9	1518	4	US-09-565-538-20	Sequence 20, Appl
C 38	51.2	10.9	2636	2	US-08-820-170A-21	Sequence 21, Appl
C 39	51.2	10.9	2636	3	US-09-055-699-21	Sequence 21, Appl
C 40	51.2	10.9	2636	4	US-09-273-565-21	Sequence 21, Appl
C 41	51.2	10.9	2636	4	US-09-565-538-21	Sequence 21, Appl
C 42	50.8	10.8	543	6	5273901-6	Patent No. 5273901
C 43	50	10.6	16442	3	US-08-781-891-208	Sequence 208, App
C 44	49.6	10.5	2369	4	US-08-910-925-2	Sequence 2, Appl
C 45	49.6	10.5	7218	1	US-08-232-463-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-09-247-155-41  
; Sequence 41, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bouqueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET 021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 41  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 68..337  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 68..124  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 10  
; OTHER INFORMATION: seq LVLLGVSIPLVSA/QN  
; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 462..467  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 482..497  
; US-09-247-155-41

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Db 142 tgtctcagctgacagctatccagctactggttcttcttctgctgctgctgctgctgctg 201
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QY 241 tcttccactgtctglaagacatttccagtttccacaaatgggttggggggtctcccgaa 300
Db 262 tcttccactgtctglaagacatttccagtttccacaaatgggttggggggtctcccgaa 321
QY 301 lqgtagagtgltccctgagatggaatccagcttcttcttcttcttcttcttcttcttct 360
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QY 361 tcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 420
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RESULT 2
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: Sequence 3, Application US/09253691
: Patent No. 6124100
: GENERAL INFORMATION:
: APPLICANT: Dong Kyu JIN
: TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
: FILE REFERENCE: 1942/36
: CURRENT APPLICATION NUMBER: US/09/253,691
: CURRENT FILING DATE: 1999-02-22
: EARLIER FILING DATE: KR 98-6,278
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: WordPerfect 6.1/Windows
: SEQ ID NO 3
: LENGTH: 397
: TYPE: DNA
: ORGANISM: human
US-09-253-691-3

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QY 135 cgtatccagctactggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 194
Db 337 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 278
QY 195 caacaactgcgacactgctgcttcccttccactgctgctgctgctgctgctgctgctgct 253
Db 277 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219

RESULT 3
US-09-135-994-1/c
: Sequence 1, Application US/09135994A
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: Patent No. 6280938
: GENERAL INFORMATION:
: APPLICANT: Ranum et al.
: TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
: FILE REFERENCE: University of Minnesota
: CURRENT APPLICATION NUMBER: US/09/135,994A
: CURRENT FILING DATE: 1998-08-18
: EARLIER FILING DATE: 1997-08-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 477
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-135-994-1

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QY 219 ctaccactgcaacacacgctgcttcttaccactgct 253
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RESULT 4
US-08-469-802B-3/c
: Sequence 3, Application US/08469802B
: Patent No. 5741645
: GENERAL INFORMATION:
: APPLICANT: Orr, Harry T.
: APPLICANT: Ranum, Laura P.W.
: APPLICANT: Chung, Ming-yi
: APPLICANT: Zoghbi, Huda Y.
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
: Patent No. 5741645
: TITLE OF INVENTION: Type 1 and Method for Diagnosis
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
: STREET: 119 No. 5741645th Fourth Street, Suite 203
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,802B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Muetting, Ann M.
: REGISTRATION NUMBER: 33,977
: REFERENCE/DOCKET NUMBER: 110.00030101
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-305-1217
: TELEFAX: 612-305-1225
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-320-559-29

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Matches 117; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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Qy 163 tgaagccctcgatgctgaaacactactgctcaacaactgagacactgctgctcctac 222
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Qy 223 cactgcaacacccgctgcttcttac 246
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Db 664 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641

RESULT 7
US-08-545-860D-29/c
; Sequence 29, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
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; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
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; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-545-860D-29

Query Match      13.8%; Score 64.8; DB 3; Length 3376;
Best Local Similarity 57.4%; Pred. No. 8.5e-10;
Matches 117; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 43 caccatgaagtcttagcagctcclgggtactccttgggagttccatcttcttgctctgc 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 844 CACTTTTATGTTCTCGAGCTCTTTAGAGGTTTTTCCTTGCTGCTCCTTCATTAATTTGT 785

Qy 103 ccagaatccgacacagctgctccagctgacacgtatccagctactggtcctgctgatga 162
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 784 GAGGCTTTGAAAACAGTGGTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725

Qy 163 tgaagccctcgatgctgaaacactactgctcaacaactgagacactgctgctcctac 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665

Qy 223 cactgcaacacccgctgcttcttac 246
    ||||| | | ||||| || |
Db 664 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641

RESULT 8
PCT-US94-04496-29/c
; Sequence 29, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/04496
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: DeLuca Esq., Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: TJU-1242
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3376 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 196..1902
: PCT-US94-04496-29

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Query Match:	13.8%;	Score	64.8;	DB	5;	Length	3376;
Best Local Similarity	57.4%;	Pred.	No.	8.5e-10;			
Matches	117;	Conservative	0;	Mismatches	87;	Indels	0; Gaps
OY	43	caccatgaagctcttcgcgctcctggactcttgaggatttccacgtttcttcgggtctctgc	102				
Db	844	CACITTTTATGTTCTCGAGTGCTTTACGAAGGTTCCTTGCTGCCTCAATAATTGT	785				
OY	103	ccagaataccgaacaagctgctccagctgcacacgatcccagctactgctgctgatga	162				
Db	784	GAGGCTTTGAAAAACTGGTACTACTGCTGCTGCTGCTGCTACTGCTGCTACTGC	725				
OY	163	tgaagcccccttgatgtgaaccactgctgtcgaaacctgcgcaactgcgtgctcctac	222				
Db	724	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	665				
OY	223	cactgcaaacaccgcgtgctctctac	246				
Db	664	TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	641				

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RESULT      9
US-09-043-303-7/c
; Sequence 7, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazujiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043.303
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 203
; TYPE: DNA
; ORGANISM: p-2093 plasmid
US-09-043-303-7

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Query Match 13.7%; Score 54.6; DB 4; Length 203;  
Best Local Similarity 59.6%; Pred. NO. 2.1e-10;  
Matches 109; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY	89	ttcttggtctctgcccagaaatccgacacacagctgtctccagctgacacgtaatccagctac	146
DB	193	TTCCGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	134
QY	149	ggtcctgctgatgtagaagccclcgatcgtaaacacactgctgctgcaacaactcgacc	208
DB	133	GCT	74
QY	209	actgctgctctaccactgcaaacacacgctgctcttaccactgctcgtaaaagacatccca	268
DB	73	GCT	14
QY	269	ggt 271	
DB	13	GTT 11	
RESULT 10			
US-08-469-802B-4/c			
: Sequence 4, Application US/08469802B			
: Patent No. 5741645			
: GENERAL INFORMATION:			
: APPLICANT: Orr, Harry T.			
: APPLICANT: Ranum, Laura P.W.			
: APPLICANT: Chung, Ming-yi			
: APPLICANT: Zoghbi, Huda Y.			
: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia			
: Patent No. 5741645			
: TITLE OF INVENTION: Type 1 and Method for Diagnosis			
: NUMBER OF SEQUENCES: 47			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.			
: STREET: 119 No. 5741645th Fourth Street, Suite 203			
: CITY: Minneapolis			
: STATE: MN			
: COUNTRY: USA			
: ZIP: 55401			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/469,802B			
: FILING DATE: 06-JUN-1995			
: CLASSIFICATION: 435			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Muetling, Ann M.			
: REGISTRATION NUMBER: 33,977			
: REFERENCE/DOCKET NUMBER: 110,00030101			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 612-305-1217			
: TELEFAX: 612-305-1225			
: INFORMATION FOR SEQ ID NO: 4:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 168 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: DNA			
US-08-469-802B-4			
Query Match 13.5%; Score 63.4; DB 1; Length 168;			
Best Local Similarity 63.4%; Pred. No. 4.4e-10;			
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps			
QY	101	gccacgaatccgcacacagctgctccagctgacacgtaatccagctactggtcctgctgat	160
DB	163	GCCTCCGAGCCCTGCTGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	104
QY	161	gatgagcccttgatgctgtagaacacactgctgctgcaacaactgacacactgctgctcct	220







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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-267-803B-2

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```

Query Match      13.5%; Score 63.4; DB 2; Length 195;
Best Local Similarity 63.4%; Pred. NO. 4.8e-10;
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 101 gccagaaatccgacacagctgctccagctgacacggtatccagctactggtcctgctgat 160
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 190 GCCCCGGAGCCCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 161 gatgaagccctgatgctgaaacacactgctgctgcaacaactgcgaccactgctgctcct 220
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 130 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 71
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 221 accactgcaaacacagctgcttctaccactgct 253
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: October 5, 2002, 05:08:26  
Job time: 4146 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 04:39:04 ; Search time 211.95 Seconds

(without alignments)

3815.365 Million cell updates/sec

Title: US-09-525-361a-23

Perfect score: 471

Sequence: 1 ctttgaagcattttgtctg.....aactatgagcgagctaacaat 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
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18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.4	99.7	471	21	AA54120
2	469.4	99.7	471	22	AAF85500
3	448.4	95.2	480	20	AA84202
4	448.4	95.2	480	21	AAC79431
5	448.4	95.2	489	20	AA00704
6	448.4	95.2	489	20	AA00644
7	448.4	95.2	497	20	AA240783
8	448.4	95.2	578	21	AAC79470
9	448.4	95.2	578	22	AA167224

10	447	94.9	482	19	AAV21992	BS106 polynucleoti
11	447	94.9	482	20	AAV55581	BS106 consensus po
12	446.8	94.9	553	19	AAV31993	BS106 polynucleoti
13	446.8	94.9	553	20	AAV55582	BS106 consensus po
14	446.4	94.8	544	21	AA291765	Human breast speci
15	446.2	94.7	472	22	AA018673	Human BS106 gene-s
16	446.2	94.7	473	22	AA018674	Human BS106 gene-s
17	443	94.1	471	22	AA265099	Membrane-bound pro
18	443	94.1	471	22	AA265099	Human PRO1160 (UNO
19	443	94.1	471	22	AA265099	Human angiogenesis
20	442.2	93.9	488	22	AA265099	Human breast. cance
21	300.8	63.9	308	19	AAV31990	BS106 polynucleoti
22	300.8	63.9	308	20	AAV55579	BS106 clone 893988
23	300.8	63.9	308	22	AA018670	Human BS106 gene-s
24	298.8	63.4	501	23	AA387721	DNA encoding novel
25	286.8	60.9	292	22	AA018671	Human BS106 gene-s
26	271.4	57.6	273	21	AA54121	Human BS106 gene-s
27	255.6	54.3	264	22	AA293399	Breast cancer prot
28	255.6	54.3	264	22	AA293399	CDNA encoding SRT
29	247.2	52.5	291	22	AA293397	CDNA encoding SRT
30	202.8	43.1	229	19	AAV31989	BS106 polynucleoti
31	202.8	43.1	229	20	AAV55578	BS106 clone 166288
32	186.4	39.6	201	22	AA018669	Human BS106 gene-s
33	181.4	38.5	197	19	AAV31991	BS106 polynucleoti
34	181.4	38.5	197	20	AAV55580	BS106 clone 120981
35	181.4	38.5	197	22	AA018672	DNA encoding novel
36	94	20.0	660	23	AA587720	Human BS106 gene-s
37	70.2	14.9	377	20	AA289891	Spinocerebellar at
38	65.4	13.9	477	21	AA244307	Human SCA7 genomic
39	65	13.8	234	16	AA084832	Spinocerebellar at
40	64.8	13.8	1326	23	AA833104	DNA encoding novel
41	64.8	13.8	3376	16	AA075166	AF-9 cDNA. 'Homo s
42	64.6	13.7	203	19	AAV30271	Glutamine rich reg
43	64.6	13.7	203	23	AAV17226	SCA2 gene CAG repe
44	64.6	13.7	1037	21	AA559242	Exons E, C and A o
45	64.6	13.7	1472	21	AA559241	Exons D, C, B and

#### ALIGNMENTS

RESULT 1  
AA54120  
ID AAA54120 standard; DNA; 471 BP.

XX AAA54120;

XX 08-FEB-2001 (first entry)

DT Breast cancer protein BCH1 coding sequence.

DE Breast cancer; diagnosis; prognosis; detection; screening.

DE Breast cancer; diagnosis; prognosis; detection; screening.

KW antibody; oestrogen receptor; anti-oestrogen; immune response;

KW lymph node; metastases; tumour; BCR3; BC08; BC05; BCH1; BCN1; BCN2;

KW BCN5; BC02; BCX2; BCX3; BCA2; BCR2; BCR7; BCY3; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 47..319

FT FT /tag= a

FT FT /product= BCH1 protein

XX WO200055629-A2.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06952.

XX 15-MAR-1999; 99US-0268865.

XX 12-NOV-1999; 99US-0439878.

XX 12-NOV-1999; 99US-0440370.

XX 15-NOV-1999; 99US-0440493.







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db 12 ctttgaagcattttgtctgtgtctccctgagatcttcagggtccaccacatgaagttcttagc 71
QY 61 agtctgtgactcttggagagttccatcttctgggtctctgcccagaatccgacaacagc 120
Db 72 agtctgtgactcttggagagttccatcttctgggtctctgcccagaatccgacaacagc 131
QY 121 tgcctcagctgacacgtatccagctactggtctctgctgagatgaagccctgagactga 180
Db 132 tgcctcagctgacacgtatccagctactggtctctgctgagatgaagccctgagactga 191
QY 181 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 240
Db 192 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 251
QY 241 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 300
Db 252 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 311
QY 301 tggtagagtgctccctgagatgaatcagcttgagcttcttgaattgggtcacacacta 360
Db 312 tggtagagtgctccctgagatgaatcagcttgagcttcttgaattgggtcacacacta 370
QY 361 ttcagcttctctgatttccatccaaactatctaccctgctcactgatatcccttttatctc 420
Db 371 ttcagcttctctgatttccatccaaactatctaccctgctcactgatatcccttttatctc 430
QY 421 taalcaatttttttttcaataaaataaactatgagcagcgtacaa 470
Db 431 taalcaatttttttttcaataaaataaactatgagcagcgtacaa 480

RESULT 6
AAX00644
ID AAX00644 standard; DNA; 489 BP.
AC AAX00644;
XX
XX
DT 25-MAR-1999 (first entry)
XX
DE Human secreted protein gene 34 clone HMQAJ64.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN W09842738-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98WO-US05311.
XX
PR 30-MAY-1997; 97US-0050937.
PR 21-MAR-1997; 97US-0041276.
PR 21-MAR-1997; 97US-0041277.
PR 21-MAR-1997; 97US-0041281.
PR 21-MAR-1997; 97US-0042344.
PR 30-MAY-1997; 97US-0048069.
PR 30-MAY-1997; 97US-0048094.
PR 30-MAY-1997; 97US-0048095.
PR 30-MAY-1997; 97US-0048096.
PR 30-MAY-1997; 97US-0048099.
PR 30-MAY-1997; 97US-0048131.
PR 30-MAY-1997; 97US-0048135.
PR 30-MAY-1997; 97US-0048154.
PR 30-MAY-1997; 97US-0048160.
PR 30-MAY-1997; 97US-0048186.
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PR 30-MAY-1997; 97US-0048187.
PR 30-MAY-1997; 97US-0048188.
PR 30-MAY-1997; 97US-0048350.
PR 30-MAY-1997; 97US-0048351.
PR 30-MAY-1997; 97US-0048352.
PR 30-MAY-1997; 97US-0048355.
PR 05-AUG-1997; 97US-0054804.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
PI Rosen CA, Ruben SM, Shi Y, Young P;
XX
XX WPI: 1999-070066/06.
XX P-PSDB: AAW67840.
XX
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1: Page 198; 385pp: English.
XX
XX This sequence represents a nucleic acid molecule which encodes a
XX secreted human protein. The gene number, and the clone it is derived
XX from, are detailed in the descriptor line. The gene can be used to
XX generate fusion proteins by linking to the gene to a human immunoglobulin
XX Fc portion (e.g. AAX00602) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 87 novel genes and their fragments (nucleic
XX acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 87
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX00611 for described uses).
XX
XX Sequence 489 BP; 125 A; 134 C; 87 G; 143 T; 0 other;
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Query Match 95.2%; Score 448.4; DB 20; Length 489;
Best Local Similarity 98.5%; Pred. No. 2e-113;
Matches 463; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 ctttgaagcattttgtctgtctccctgagatcttcagggtccaccacatgaagttcttagc 60
Db 9 ctttgaagcattttgtctgtctccctgagatcttcagggtccaccacatgaagttcttagc 68
QY 61 agtctgtgactcttggagagttccatcttctgggtctctgcccagaatccgacaacagc 120
Db 69 agtctgtgactcttggagagttccatcttctgggtctctgcccagaatccgacaacagc 128
QY 121 tgcctcagctgacacgtatccagctactggtctctgctgagatgaagccctgagactga 180
Db 129 tgcctcagctgacacgtatccagctactggtctctgctgagatgaagccctgagactga 188
QY 181 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 240
Db 189 aaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 248
QY 241 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 300
Db 249 tctaccactgctgctgcaacaactcgaccactgctgctctctaccactgcaaccaccgctgc 308
QY 301 tggtagagtgctccctgagatgaatcagcttgagcttcttgaattgggtcacacacta 360
Db 309 tggtagagtgctccctgagatgaatcagcttgagcttcttgaattgggtcacacacta 367
QY 361 ttcagcttctctgatttccatccaaactatctaccctgctcactgatatcccttttatctc 420
Db 368 ttcagcttctctgatttccatccaaactatctaccctgctcactgatatcccttttatctc 427
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QY 421 taatcagtttattttcttctcaaaataaataaactatgagcgagctaaca 470  
|||||  
Db 428 taatcagtttattttcttctcaaaataaataaactatgagcaaaaaa 477

RESULT 7  
AAZ40783  
ID AAZ40783 standard; DNA; 497 BP.  
AC AAZ40783;  
XX  
XX  
DT 18-JAN-2000 (first entry)  
XX  
DE Secreted protein EST coding sequence 108-002-5-0-F3-FL.  
XX  
KW Secreted protein; fingerprint identification technique;  
KW chromosome mapping; human; hereditary disease; diagnosis; cancer;  
KW hyperlipidaemia; cardiovascular; neurodegenerative disorder; therapy;  
KW autoimmune disease; rheumatic disease; embryogenic disorder; myopathy;  
KW renal injury; amino aciduria; hypoglycaemia; male rat infertility;  
KW hypertension; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9940189-A2.  
XX  
XX 12-AUG-1999.  
XX  
XX 09-FEB-1999; 99WO-1B00282.  
XX  
XX 09-FEB-1998; 98US-0074121.  
XX 13-APR-1998; 98US-0081563.  
XX 10-AUG-1998; 98US-0096116.  
XX 04-SEP-1998; 98US-0099273.  
XX  
XX (CEST ) GENSET.

PA Bougueleret L, Duclert A, Dumas Milne Edwards J;  
PJ  
XX  
XX WPI; 1999-600966/51.  
XX P-PSDB; AAY59655.  
XX  
XX Extended cDNAs useful for expressing secreted proteins and to obtain  
XX specific antibodies -  
XX  
XX Claim 1: Page 150; 244pp; English.  
XX  
XX This sequence encodes a human secreted protein of the invention. The  
XX extended cDNAs (or genomic DNAs obtainable from them) may be used to  
XX prepare PCR primers and probes. These are useful for forensic matching or  
XX positive identification by DNA sequencing. They may also be used in  
XX alternative fingerprint identification techniques. Antibodies against the  
XX proteins encoded by the extended cDNAs are useful in identification of  
XX tissue types or cell species, as well as identifying tissue specific  
XX soluble proteins. The sequences can be used for chromosome mapping and  
XX identification of genes associated with hereditary diseases or drug  
XX response. Signal sequences from the cDNAs can be used in construction of  
XX secretion vectors. Other sequences derived from the extended cDNAs can be  
XX used to clone upstream genomic DNA sequences including promoters. This is  
XX in turn useful for identifying proteins that interact with promoter  
XX sequences. Some of the proteins may be useful in diagnosing and treating  
XX several disorders including, but not limited to: cancer, hyperlipidaemia,  
XX cardiovascular and neurodegenerative disorders, autoimmune diseases, and  
XX rheumatic diseases, embryogenic disorders, hypertension, renal injury,  
XX amino acidurias, hypoglycaemia, male rat infertility and myopathies.  
XX  
XX Sequence 497 BP; 122 A; 138 C; 90 G; 147 T; 0 other;

Query Match 95.2%; Score 448.4; DB 20; Length 497;  
Best Local Similarity 98.5%; Pred. No. 2e-113;  
Matches 463; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ctttgaagcattttttgtctgtcctcctgatctctcaggtccaccaccatgaagttcttlayc 60  
|||||  
Db 22 ctttgaagcattttttgtctgtcctcctgatctctcaggtccaccaccatgaagttcttlayc 81  
QY 61 agtctcgttactcttgggagtttccatcttcttggctctgccagaatccgacaacagc 120  
|||||  
Db 82 agtctcgttactcttgggagtttccatcttcttggctctgccagaatccgacaacagc 141  
QY 121 tgcctccagctgacagctatccagctactggtcctctgatgatgaagccctgatgctga 180  
|||||  
Db 142 tgcctccagctgacagctatccagctactggtcctctgatgatgaagccctgatgctga 201  
QY 181 aacctgctgctgcaacaacgacgacctgctgctctaccactgcaaccaccgctgc 240  
|||||  
Db 202 aacctgctgctgcaacaacgacgacctgctgctctaccactgcaaccaccgctgc 261  
QY 241 ttctaccactgctcgtaaagacattccagtttaccacaaatgggtgggagatccccgaa 300  
|||||  
Db 262 ttctaccactgctcgtaaagacattccagtttaccacaaatgggtgggagatccccgaa 321  
QY 301 tggtagagtgtcctcctgagatggaatcagcttgagttcttgcattgggtgcacaacta 360  
|||||  
Db 322 tggtagagtgtcctcctgagatggaatcagcttgagttcttgcattgggtgcacaacta 380  
QY 361 ttcatgcttctcctggtatttccatccaaactacttacccttgctcagatccccctttatctc 420  
|||||  
Db 381 ttcatgcttctcctggtatttccatccaaactacttacccttgctcagatccccctttatctc 440  
QY 421 taatcagtttattttcttccaaataaaaaataactatgagcgagctaaca 470  
|||||  
Db 441 taatcagtttattttcttccaaataaaaaataactatgagcaaaaaaaa 490

RESULT 8  
AAC79470  
ID AAC79470 standard; cDNA; 578 BP.  
XX  
XX AAC79470;  
XX  
XX 07-FEB-2001 (first entry)  
XX  
XX cDNA sequence of human breast tumour clone B511S.  
XX Human; breast tumour antigen; cytostatic; immunotherapy;  
KW breast cancer; vaccine; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200061756-A2.  
XX 19-OCT-2000.  
XX 10-APR-2000; 2000WO-US09688.  
XX 09-APR-1999; 99US-0288950.  
XX 02-JUL-1999; 99US-0346327.  
XX (CORI-) CORIXA CORP.  
XX  
XX Reed SG, Xu J, Dillon DC;  
XX  
XX WPI; 2000-638568/61.  
XX P-PSDB; AAB28525.  
XX  
XX A novel isolated polypeptide comprising an immunogenic portion of a  
XX breast cancer protein useful in the detection and treatment of breast  
XX cancer -  
XX  
XX Claim 4; Page 88; 95pp; English.

XX  
XX The present sequence was isolated from a breast tumour cDNA library. It  
XX is provided in a specification relating to compounds for immunotherapy



and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.

Query Match	95.2%	Score 448.4;	DB 21;	Length 578;
Best Local Similarity	98.5%	Pred. No. 2.2e-113;		
Matches 463;	Conservative	0;	Mismatches 6;	Indels 11;
Gaps 1;				

QY	1	ctttgaagca	cttttctgtgctccctgattcttcaggtcacacacatgaagtctttagc	60
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Db	77	agtccttggtactcttgggagtttccacattctctggtctctgccagaaatccgacacagc	136	
QY	121	tgtctcagctgacacatataccagctactggtctgtgatgaagcccttgactgcta	180	
Db	137	tgtctcagctgacacgtataccagctactggtctgtgatgaagcccttgactgcta	196	
QY	181	aaccactgtctgtgcaacaaactgcgaccactgtctctctaacctgcaacacagctgc	240	
Db	197	aaccactgtctgtgcaacaaactgcgaccactgtctctctaacctgcaacacagctgc	256	
QY	241	tctacacactgtctgtaagagacattccagttttaccacaaatgggttggggatctcccgaa	300	
Db	257	tctacacactgtctgtaagagacattccagttttaccacaaatgggttggggatctcccgaa	316	
QY	301	tgttagagatgtgctccttgagatggaaatcagcttgtagctcttgcaattctgggttcacaaacta	360	
Db	317	tgttagagatgtgctccttgagatggaaatcagcttgtagctcttgcaattt-ggtcacaacta	375	
QY	361	tctcatgcttctcttgatattccatccaaactactaaccttgcctcagatccccctttatcttc	420	
Db	376	tctcatgcttctcttgatattccatccaaactactaaccttgcctcagatataccccctttatcttc	435	
QY	421	taatacagtttatttttcttcaataaaaaataactatgagcgagctaaaca	470	
Db	436	taatacagtttatttttcttcaataaaaaataactatgagcgacaaaga	485	

RESULT 9  
AAI67224  
ID AAI67224 standard; cDNA: 578 BP.

AA  
AC  
AA167224:

DT 11-FEB-2002 (first entry)

DE B511S cDNA sequence.

Genetic subtraction; DNA microarray analysis; polymerase chain reaction; cancer; B511S; ss.

OS Homo sapiens.

```

key      Location/Qualifiers
CDS      63..335
          /*tag= a

```

PN WO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR	20-JUL-2000; 2000US-219862P.	
PR	27-JUL-2000; 2000US-221300P.	
PR	18-DEC-2000; 2000US-256592P.	
XX		
XX	(CORI-) CORIXA CORP.	
XX		
PI	Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;	
XX	WPI; 2001-626449/72.	
DR	P-PSDB; AAG65988.	
DR		
XX		
PT	Identifying tissue (tumour)-specific polynucleotides overexpressed in	
PT	tissue of interest as compared to control tissue, for detecting cancer	
PT	cells in patient, comprises DNA microarray analysis or quantitative	
PT	polymerase chain reaction -	
XX		
PS	Claim 4; Page 116; 127pp; English.	
XX		
CC	The invention relates to identifying tissue-specific polynucleotides (P)	
CC	that involves performing a genetic subtraction to identify pool of (P)	
CC	from tissue of interest (TI), performing DNA microarray analysis to	
CC	identify first subset of polynucleotides (SP1) at least 2-fold over	
CC	expressed in TI, and performing quantitative polymerase chain reaction	
CC	(PCR) analysis on SP1 to identify second subset of (P). The method is	
CC	useful for determining the presence or absence of a cancer cell in a	
CC	patient, monitoring the progression of cancer in a patient using a	
CC	biological sample such as blood, serum, lymph nodes, bone marrow, sputum,	
CC	urine or a tumour biopsy sample. The methods are useful for determining	
CC	the presence or absence of or monitoring progression of prostate, breast,	
CC	colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,	
CC	gastric, kidney, bladder, pancreatic or endometrial cancer. The present	
CC	sequence represents B5115 CDNA.	
XX		
QQ	Sequence 578 BP; 206 A; 137 C; 88 G; 147 T; 0 other;	

Query Match	95.2%;	Score 448.4;	DB 22;	Length 578;
Best Local Similarity	98.5%;	Pred. No. 2.2e-113;		
Matches 463;	Conservative 0;	Mismatches 6;	Indels 1;	

Qy	1	ctttgaagcatttttgtctgtctccctgatctctcaggtccaccaccatgaagtctcttagc	60
Db	17	ctttgaagcatttttgtctgtctccctgatctctcaggtccaccaccatgaagtctcttagc	76
Qy	61	agtcctggtactcttggagagtttccattcttctggtctcttgcgccagaaatccgacaaacgc	120
Db	77	agtcctggtactcttggagagtttccattcttctggtctcttgcgccagaaatccgacaaacgc	136
Qy	121	tgtctcagctgacacgtatccagctactcagcttcttgccttgcctgatgatgaagcccttgatctga	180
Db	137	tgtctcagctgacacgtatccagctactcagcttcttgccttgcctgatgatgaagcccttgatctga	196
Qy	181	aaccacttgcctgtcgaacaactgcgacacactgtgccttccactgcacaccacgcctgc	240
Db	197	aaccacttgcctgtcgaacaactgcgacacactgtgccttccactgcacaccacgcctgc	256
Qy	241	tctaccacttgcctgtcgaagaacatccagttttaccacaaaatgggttggggatctcccga	300
Db	257	tctaccacttgcctgtcgaagaacatccagttttaccacaaaatgggttggggatctcccga	316
Qy	301	tggtagagtggtcccttgaagtgaatcagcttgagttcttgcgaattgggtccacaacta	360
Db	317	tggtagagtggtcccttgaagtgaatcagcttgagttcttgcgaattt-ggtccacaacta	375
Qy	361	tctatgcttctctgtgatttcataccaactacttaccttgcctcagatataccccctttatctc	420
Db	376	tctatgcttctctgtgatttcataccaactacttaccttgcctcagatataccccctttatctc	435
Qy	421	taatcagtttattttcttccaaaataaaaaataactatgagcgagctaa	470
Db	436	taatcagtttattttcttccaaaataaaaaataactatgagcaacaaga	485







PF 28-FEB-2001; 2001WO-US06516.  
 XX  
 PR 29-FEB-2000; 2000US-0516444.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;  
 PI Russell JC, Stroupe SD;  
 XX  
 DK WPI; 2001-596773/67.  
 XX  
 PT A gene or its fragment which codes for a BS106 polypeptide, useful for  
 PT the detection of a breast disease such as breast cancer -  
 XX  
 PS Example 1; Fig 1; 158pp; English.  
 XX  
 CC The invention relates to human BS106-specific polypeptides and  
 CC polynucleotides. The BS106 polypeptides and antibodies are useful  
 CC for detecting, diagnosing, staging, monitoring, prognosticating,  
 CC preventing, treating or determining the predisposition of an  
 CC individual to diseases and conditions of the breast such as breast  
 CC cancer. They are also useful in the treatment of tumours or  
 CC metastases. Polynucleotides of the invention are useful in drug  
 CC screening and gene therapy. The present sequence is human BS106  
 CC gene specific full length cDNA, expressed sequence tag (EST) clone  
 CC 1662885inh.  
 XX  
 SQ Sequence 472 BP; 108 A; 134 C; 86 G; 144 T; 0 other;

Query Match 94.7%; Score 446.2; DB 22; Length 472;  
 Rust Local Similarity 99.1%; Pred. No. 8e-113;  
 Matches 459; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 ctttgaagcattttgtctgtcctcctgatcttcaggctcaccacccatgaagtctctagc 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 9 ctttgaagcattttgtctgtcctcctgatcttcaggctcaccacccatgaagtctctagc 68  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 61 agtctcctggtactcttggggagttccatctttctgttctgtcccgaaatccgacacagc 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 69 agtctcctggtactcttggggagttccatctttctgttctgtcccgaaatccgacacagc 128  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 121 tgcctcagctgacacgtatccagctactgctcctcctgctgatgatgaagccctgagtctga 180  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 129 tgcctcagctgacacgtatccagctactgctcctcctgctgatgatgaagccctgagtctga 188  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 181 aaccactgctgctgcaacactgacacccactgctcctcctaccactgcaaccacgcctgc 240  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 189 aaccactgctgctgcaacactgacacccactgctcctcctaccactgcaaccacgcctgc 248  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 241 ttctaccactgctcgttaagagacattccagttttaccacaaatgggttggggatctcccgaa 300  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 249 ttctaccactgctcgtlaagagacattccagttttaccacaaatgggttggggatctcccgaa 308  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 301 tggtagagtgctccctgagatggaatcagcttgagcttcttgcgaattgggtgcacaaacta 360  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 309 tggtagagtgctccctgagatggaatcagcttgagcttcttgcgaatt-ggtcacaaacta 367  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 361 ttcatgcttccctgctgatttcacccaactacttaccttgcctacgatatcccttttatctc 420  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 368 ttcatgcttccctgctgatttcacccaactacttaccttgcctacgatatcccttttatctc 427  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 421 taatcagtttatttttttccaaataaaaaataactatgagcga 463  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 428 taatcagtttatttttttccaaataaaaaataactatgagcga 470  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 04:00:45 ; Search time 1900.29 Seconds  
(Without alignments)  
5186.787 Million cell updates/sec

Title: US-09-525-361A-23

Perfect score: 471  
Sequence: 1 cttgaagcatttcgtctg.....aactatgacgagctaacat 471

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_com: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_to: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match length DB ID Description  
No. Score

1	448.4	95.2	497	6	AR177347	AR177347 Sequence
2	448.4	95.2	578	6	AX282981	AX282981 Sequence
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4	446.8	94.9	553	6	BD007432	BD007432 Reagent a
5	446.2	94.7	472	6	AX240679	AX240679 Sequence
6	446.2	94.7	473	6	AX240680	AX240680 Sequence
7	445.4	94.6	472	6	AX328498	AX328498 Sequence
8	442.2	93.9	488	6	AX067322	AX067322 Sequence
9	383.4	81.4	396	6	AF141087	AF141087 Homo sapi
10	300.8	63.9	308	6	AX240676	AX240676 Sequence
11	300.8	63.9	308	6	BD007429	BD007429 Reagent a
12	286.8	60.9	292	6	AX240677	AX240677 Sequence
13	269.8	57.3	273	6	AX328499	AX328499 Sequence
14	255.6	54.3	264	6	AX079476	AX079476 Sequence
15	255.6	54.3	265	6	AX079475	AX079475 Sequence
16	247.2	52.5	291	6	AX079474	AX079474 Sequence
17	202.8	43.1	229	6	BD007428	BD007428 Sequence
18	187	39.7	133000	2	AC079842	AC079842 Homo sapi
19	187	39.7	188873	2	AC019223	AC019223 Homo sapi
20	187	39.7	222877	2	AC024091	AC024091 Homo sapi
21	186.4	39.6	201	6	AX240675	AX240675 Sequence
22	181.4	38.5	197	6	AX240678	AX240678 Sequence
23	181.4	38.5	197	6	BD007430	BD007430 Reagent a
24	80.8	17.2	469	10	RATSP071	M33976 Rat salivary
25	70.2	14.9	397	6	BD010479	BD010479 Diagnostic
26	69.6	14.8	1591	10	RNO6295	AJ006295 RatLus no
27	69.6	14.8	68409	2	AC105975	AC105975 Mus muscu
28	69.6	14.8	185363	2	AC094466	AC094466 RatLus no
29	69.4	14.7	5727	2	AY045719	AY045719 Latus alic
30	68.8	14.6	666	8	AF413050S2	AF413051 Zea mays
31	68.8	14.6	46904	2	AC100911	AC100911 Mus muscu
32	67.8	14.4	98221	2	AC097839	AC097839 RatLus no
33	67.6	14.4	155780	9	HS336012	AL513498 Homo sapi
34	67.6	14.4	175695	2	AL606844	AL606844 Homo sapi
35	67.2	14.3	180668	2	AC020857	AC020857 Mus muscu
C 36	66.8	14.2	110000	2	AC092202_1	Continuation (2 of
C 37	66.8	14.2	173851	2	AC096966	AC096966 RatLus no
C 38	66.8	14.2	204152	2	AC092203	AC092203 Mus muscu
C 39	66.6	14.1	2960	3	AY057052	AY057052 Mamestra
40	66.4	14.1	624	3	AF139019	AF139019 Cepaea ne
41	66.4	14.1	236962	2	AL606742	AL606742 Mus muscu
42	66.2	14.1	223398	5	FR0271723	AJ2271723 Fugu rubr
C 43	66.2	14.1	229380	2	AC079636	AC079636 Mus muscu
44	66	14.0	5719	10	MMCAT51	AF051726 Mus muscu
45	66	14.0	27613	9	AC002053	AC002053 Cosmid c1

ALIGNMENTS

RESULT 1	AR177347	497 bp	DNA	linear	PAT 17-TRC-2001
LOCUS	AR177347	Sequence 41 from patent US 6312922.			
DEFINITION	AR177347				
ACCESSION	AR177347				
VERSION	AR177347.1	GI:17919702			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 497)				
AUTHORS	Edwards,J.-R.,Dumas,MJine., Duclet,A. and Bouguetelert,J..				
TITLE	Complementary DNAs				
JOURNAL	Patent: US 6312922-A 41 06-NOV-2001;				
FEATURES	Location/Qualifiers				
source	1..497				
BASE COUNT	122 a 138 c 90 g 147 t				
ORIGIN	/organism="unknown"				

Query Match 95.2% Score 448.4; DB 6; Length 497;  
Best Local Similarity 98.5%: Pred. No. 1.6e-96;

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Db	22	cttttaagacatttttgcctgctctccctcctatcttagcgcacacacattgaattcttagc	81			
OY	61	agtcctggaacctcttggaagattccatctcttcctgctctcgcgaagatccgaacagc	120			
Db	82	agtcctggaacctcttggaagattccatctcttcctgctctcgcgaagatccgaacagc	141			
OY	121	tgctccagctgacacgataccagactactggtccctgctgatagaagaagccctgatactga	180			
Db	142	tgctccagctgacacagatgataccagactgctgctgctgctgctgctgctgctgctgctg	201			
OY	181	aaccacgtctgcttggaagaacactggaagacacactgctcctaccactgcaacacgcgtgc	240			
Db	202	aaccacgtctgcttggaagaacactggaagacacactgctcctaccactgcaacacgcgtgc	261			
OY	241	ttctaaccaactgctcgtlaaagacatctcaagttcttaccacaataggtcttggaatctccgaa	300			
Db	262	ttctaaccaactgctcgtlaaagacatctcaagttcttaccacaataggtcttggaatctccgaa	321			
OY	301	tggttagatgtgtccctcgagatgagatacagcttgtagtctcttcgcaatttggtcacaacta	360			
Db	322	tggttagatgtgtccctcgagatgagatacagcttgtagtctcttcgcaatttggtcacaacta	380			
OY	361	ttcaagcttccctgtaatttcaaccacaacttaacttgctcgtacgatactccctttatctc	420			
Db	381	ttcaagcttccctgtaatttcaaccacaacttaacttgctcgtacgatactccctttatctc	440			
OY	421	taactcaatttattctctcttcaaaataaaataactatgagcagactaaca	470			
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	Matches	463: Conservative	0: Mismatches	6: Indels	1: Gaps	1:
OY	1	cttgaagacattcttgctcgtgcctccgacatctcaagtcaccacatgaagttcttagc	60			
Db	22	cttttaagacatttttgcctgctctccctcctatcttagcgcacacacattgaattcttagc	81			
OY	61	agtcctggaacctcttggaagatctcactctcttcctgctctcgcgcgaatccgaacaagc	120			
Db	82	agtcctggaacctcttggaagatctcactctcttcctgctctcgcgcgaatccgaacaagc	141			
OY	121	tgctccagctgacacgatatccagctactggtccctgctgatagaagaagccctgatactga	180			
Db	142	tgctccagctgacacagatgataccagctactggtccctgctgatagaagaagccctgatactga	201			
OY	181	aaccacgtctgcttggaagaacactgagacacactgctcctctaccactgcaacacgcgtgc	240			
Db	202	aaccacgtctgcttggaagaacactgagacacactgctcctctaccactgcaacacgcgtgc	261			
OY	241	ttctaaccaactgctcgtlaaagacatctcaagttcttaccacaataggtcttggaatctccgaa	300			
Db	262	ttctaaccaactgctcgtlaaagacatctcaagttcttaccacaataggtcttggaatctccgaa	321			
OY	301	tggtagaatggtgctccctgagatgagatacagctctgagctctctgcgaattggtctacaacta	360			
Db	322	tggtagaatggtgctccctgagatgagatacagctctgagctctctgcgaattggtctacaacta	380			
OY	361	ttcaagctctccgtgattcttaccacaacacttaacttgctcctcagatataccctcttatctc	420			
Db	381	ttcattgctctccgtgattcttaccacaacacttaacttgctcctcagatataccctcttatctc	440			
OY	421	taactcaatttatctctcttccaaataaataaactatgagcagactaaca	470			
Db	441	taactcaatttatctctcttccaaataaataaactatgagcagactaaca	490			

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OY 1 cttggaagcattttgtctgtgtccctgtatcttcaggtaccacatgaaagttcttagc 60
|||||
DB 18 ctttgaagcattttgtctgtgtccctgtatcttcaggtaccacatgaaagttcttagc 77
61 agtccgtgactccttgggaagttccatctcttcgtgtctgtcccaagaatccgaacagc 120
|||||
DB 78 agtccgtgactccttgggaagttccatctcttcgtgtctgtcccaagaatccgaacagc 137
121 tgcctcagctgacagbataccagctactgtgtctgtctgtatgataagccctgtatgta 180
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DB 138 tgcctcagctgacagbataccagctactgtgtctgtctgtatgataagccctgtatgta 197
181 aaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 240
|||||
DB 198 aaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 257
241 tctaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 300
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DB 258 tttctaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 317
OY 301 tggtagagtggtgtccctgagatggaatcagctgagctcttcgtcaattgggtacaacla 360
318 tggtagagtggtgtccctgagatggaatcagctgagctcttcgtcaattgggtacaacla 376
DB 361 ttcagctctcctgtgtatcttccaaactacttaccctgtgctcagatatacccttattctc 420
377 tttatctcttctgtgtatcttccaaactacttaccctgtgctcagatatacccttattctc 436
OY 421 taatcagttattcttcttcaataaaataactatgaagcga 463
437 taatcagttattcttcttcaataaaataactatgaagcga 479
DB 437 taatcagttattcttcttcaataaaataactatgaagcga 479

RESULT 4
LOCUS BD007432 553 bp DNA linear PAT 31-JAN-2002
DEFINITION Reagent and method useful in detecting mammary diseases.
ACCESSION BD007432
VERSION BD007432.1 GI:18635803
KEYWORDS JP 2001503980-A/5.
SOURCE unclassified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 553)
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
Russell,J.C. and Stroupe,S.D.
Reagent and method useful in detecting mammary diseases
Patent: JP 2001503980-A 5 27-MAR-2001;
ABBOTT LABORATORIES
COMMENT OS Unidentified
PN JP 2001503980-A/5
PD 27-MAR-2001
PF 31-OCT-1997 JP 1998520795
PR 31-OCT-1996 US 08/742067
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI
POLA N FRIEDMAN,
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI MICHAEL
R KLASS,
PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI
STEVEN D STROUPE
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47,
PC C07K16/30,
PC C12N5/10,C12P21/02,C12O1/68,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..553
Location/Qualifiers
1..553
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BASE COUNT 159 a 144 c 101 g 148 t 1 others
ORIGIN
Query Match 94.9%; Score 446.8; DB 6; Length 553;
Best Local Similarity 98.3%; Pred. No. 3,9e-96;
Matches 462; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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61 agtccgtgactccttgggaagttccatctcttcgtgtctgtcccaagaatccgaacagc 120
DB 92 agtccgtgactccttgggaagttccatctcttcgtgtctgtcccaagaatccgaacagc 151
121 tgcctcagctgacagbataccagctactgtgtctgtctgtatgataagccctgtatgta 180
DB 152 tgcctcagctgacagbataccagctactgtgtctgtctgtatgataagccctgtatgta 211
OY 181 aaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 240
DB 212 aaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 271
OY 241 tctaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 300
DB 272 tttctaccactgtcgtcgtgaacaacatcgtgcacactgtctgtctcaccacgtgcaacacgcgtgc 331
377 tttatctcttctgtgtatcttccaaactacttaccctgtgctcagatatacccttattctc 436
OY 421 taatcagttattcttcttcaataaaataactatgaagcga 470
437 taatcagttattcttcttcaataaaataactatgaagcga 500
DB 437 taatcagttattcttcttcaataaaataactatgaagcga 500

RESULT 5
LOCUS AX240679 472 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 5 from Patent WO0165262.
ACCESSION AX240679
VERSION AX240679.1 GI:15797662
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 472)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the breast
Patent: WO 0165262-A 5 07-SEP-2001;
ABBOTT LABORATORIES (US)
COMMENT OS Unidentified
PN JP 2001503980-A/5
PD 27-MAR-2001
PF 31-OCT-1997 JP 1998520795
PR 31-OCT-1996 US 08/742067
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI
POLA N FRIEDMAN,
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI MICHAEL
R KLASS,
PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI
STEVEN D STROUPE
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47,
PC C07K16/30,
PC C12N5/10,C12P21/02,C12O1/68,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..472
Location/Qualifiers
1..472
BASE COUNT 108 a 134 c 86 g 144 t
ORIGIN
Query Match 94.7%; Score 446.2; DB 6; Length 472;
Best Local Similarity 99.1%; Pred. No. 5,4e-96;
Matches 459; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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OY 1 cttgaagcatttctgtctgtccctgaltcctcaagcaacatgaagttcttagc 60  
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DB 9 CTTTGAAGCATTTTTGTCTGTCTCCCTGATCTTCATGTACACCACTGAAGTTCTTAGC 68  
OY 61 agtctgtactcttgggaatttccactcttctgtctctgcccagaatccgcgaagc 120  
|||||  
DB 69 AGTCTGTACTCTTGGGAGCTTTCATCTTGTGCTCTGCCAGAAATCCGCAACAGC 128  
OY 121 tgcctcagctgacacagatccagctactggtccctctgcatgataagaaacccctatgctga 180  
|||||  
DB 129 TGCTCCAGCTGACACGATACAGTACTGCTCTGCTGATGATGAACCCCTGATGCTGA 188  
OY 181 aacacatgctgctgacaaacatcgacacactgctgtctctaccatctgcaacacccgctgc 240  
|||||  
DB 189 AACCACTGCTGTCGCAACCACTGCGACACTGCTGCTCCACCACTGCAACCAACCGCTGC 248  
OY 241 ttcacacatgctgctgaaagacatccagtttccaaatgggttgggaattcccgaa 300  
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DB 249 TTCTACCACTGCTGCTGAACACATTCAGTTTACCCAAATGGGTGGGATCTCCCGAA 308  
OY 301 tggtagaagtgctccctgagaatgaatcaagcttgaagctctctgcaattgggtcacacta 360  
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DB 309 TGCTAGAGTGTGTCCCTGAGATGGAATCAGCTTGAGTCTTCTGCAATT-GGTCAACAATA 367  
OY 361 ttcacgtcttcctgtgattcaccacactactacactgctgctacgatatcccttattctc 420  
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DB 368 TTGATGCTTCTGATTTATCTCACTACCTTACCTTGCTGATGATATCCCTTTATCTC 427  
OY 421 taatcagttattcttctcaataaataactatgaagcga 463  
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DB 428 TAATCAGTTTATTTCTTTCATAATTAATAACTATGAGCAA 470

RESULT 6  
LOCUS AX240680 473 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 6 from Patent WO0165262.  
ACCESSION AX240680  
VERSION AX240680.1 GI:15797663  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 473)  
AUTHORS Billing-Medel, P.A., Cohen, M., Golplitz, T.L., Friedman, P.N.,  
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,  
Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.  
TITLE Reagents and methods useful for detecting diseases of the breast  
JOURNAL Patent: WO 0165262-A 6 07-SEP-2001;  
ABBOTT LABORATORIES (US)  
FEATURES  
source location/Qualifiers  
1..473  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 108 a 134 c 86 g 145 t  
ORIGIN

Query Match 94.7%; Score 446.2; DB 6; Length 473;  
Best Local Similarity 99.1%; Pred. No. 5.4e-96;  
Matches 459; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
OY 1 cttgaagcatttctgtctgtccctgaltcctcaagcaacatgaagttcttagc 60  
|||||  
DB 9 CTTTGAAGCATTTTTGTCTGTCTCCCTGATCTTCATGTACACCACTGAAGTTCTTAGC 68  
OY 61 agtctgtactcttgggaatttccactcttctgtctctgcccagaatccgcgaagc 120  
|||||  
DB 69 AGTCTGTACTCTTGGGAGCTTTCATCTTGTGCTCTGCCAGAAATCCGCAACAGC 128  
OY 121 tgcctcagctgacacagatccagctactggtccctctgcatgataagaaacccctatgctga 180  
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DB 129 TGCTCCAGCTGACACGATATCCAGCTACTGCTGCTGCTGATGATGAAGCCCTGATGCTTGA 188  
OY 181 aacacatgctgctgacaaacatcgacacactgctgtcttccacacatgaagcagctgac 240  
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DB 189 AACCACTGCTGTCGCAACCACTGCGACACTGCTGCTCCACCACTGCAACCAACCGCTGC 248  
OY 241 ttcacacatgctgctgaaagacatccagtttccaaatgggttgggaattcccgaa 300  
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DB 249 TTCTACCACTGCTGCTGAACACATTCAGTTTACCCAAATGGGTGGGATCTCCCGAA 308  
OY 301 tggtagaagtgctccctgagaatgaatcaagcttgaagctctctgcaattgggtcacacta 360  
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DB 309 TGCTAGAGTGTGTCCCTGAGATGGAATCAGCTTGAGTCTTCTGCAATT-GGTCAACAATA 367  
OY 361 ttcacgtcttcctgtgattcaccacactactacactgctgctacgatatcccttattctc 420  
|||||  
DB 368 TTGATGCTTCTGATTTATCTCACTACCTTACCTTGCTGATGATATCCCTTTATCTC 427  
OY 421 taatcagttattcttctcaataaataactatgaagcga 463  
|||||  
DB 428 TAATCAGTTTATTTCTTTCATAATTAATAACTATGAGCAA 470

RESULT 7  
LOCUS AX328498 472 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 1 from Patent WO0135811.  
ACCESSION AX328498  
VERSION AX328498.1 GI:18098424  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Mack, D. and Gish, K.C.  
TITLE Novel methods of diagnosing and determining prognosis of breast  
cancer, compositions, and methods of screening for breast cancer  
modulators  
JOURNAL Patent: WO 0135811-A 1 25-MAY-2001;  
EOS Biotechnology, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..472  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 109 a 132 c 88 g 143 t  
ORIGIN

Query Match 94.6%; Score 445.4; DB 6; Length 472;  
Best Local Similarity 99.2%; Pred. No. 8.4e-96;  
Matches 469; Conservative 0; Mismatches 1; Indels 2;  
OY 1 cttgaagcatttctgtctgtccctgaltcctcaagcaacatgaagttcttagc 60  
|||||  
DB 1 CTTTGAAGCATTTTTGTCTGTCTCCCTGATCTTCAGCTGACCAACATGAAGTTCTTAGC 60  
OY 61 agtctgtg--taacttgggaattcactcttctgtctctgcccagaatccgcgaagc 118  
|||||  
DB 61 AGTCTGTACTCTTGGGAGCTTTCATCTTGTGCTCTGCCAGAAATCCGCAACGA 119  
OY 119 gctgtcagctgacacagatccagctactggtccctctgcatgataagaaacccctatgct 178  
|||||  
DB 120 GCTGCTCCAGCTGACACGATACAGTACTGCTGCTGATGATGAAGCCCTGATGCT 179  
OY 179 gaaacacatgctgctgaaacacatcgacacactgctgtctccacacacagcaacacacccct 218  
|||||  
DB 180 GAAACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTTACCACTGCAACCAACCGCT 219  
OY 239 gcttccacacatgctgtaaaagacatccaaatllacccaagtgatgggaatcttcttcttctt 298  
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DB 240 GCTTACACACTGCTGCTGAACACATTCAGCTTTTACCCAAATGGGTGGGATGCTTCTGCTG 299  
|||||

Query Match	93.9%: Score 442.2; DB 6; Length 488;	Best Local Similarity 98.3%: Pred. No. 4.9e-95;	Matches 455; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
OY 299	aatggaagagtgctgtcccgagatggaatcaacattgagctcttcgaaatggtgacaac	358	
DB 300	aaatggaagagtgctgtcccgagatggaatcaacattgagctcttcgaaatggtgacaac	359	
OY 359	tattcagcttcctgagattccatccaacttacttacctgctctagatatacccttatac	418	
DB 360	tattcagcttcctgagattccatccaacttacttacctgctctagatatacccttatac	419	
OY 419	lcthaacagtttattcttcttccaataaaaaaataactagagcagatcaaat	471	
DB 420	tctaatcagtttattcttcttccaataaaaaaataactagagcagatcaaat	472	
RESULT 8			
AX067322	AX067322	488 bp	DNA
LOCUS	Sequence 26 from Patent WO0078960.		Linear
DEFINITION	AX067322		PAT 24-JAN-2001
ACCESSION	AX067322.1		
VERSION	GI:12544946		
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Yuglu,J.J. and Mitcham,J.L.		
JOURNAL	Compositions and methods for the therapy and diagnosis of breast		
FEATURES	Patent: WO 0078960-A 26 28-DEC-2000;		
SOURCE	CORIXA CORPORATION (US)		
BASE COUNT	Location/Qualifiers		
ORIGIN	1..488		
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	/db_xref="taxon:9606"		
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DB 1	gcattttgtctgtctccctgatacttcgaagtcacacatgaagctcttagcagctc	60	
OY 68	gtaacctgtggaagtttccatcttctgtctctgctcgcgaagtcacgaacacagctgtcca	127	
DB 61	gtactcttggggagtttccatcttctgtctctgctcgcgaagtcacgaacacagctgtcca	120	
OY 128	gctgacagctacccagctcgtctcgtcgtatgataagacccctgagctgtgaaacct	187	
DB 121	gctgacagctacccagctcgtctcgtcgtatgataagacccctgagctgtgaaacct	180	
OY 188	gctgctgcaacaactcgtgacacacgtgctcctcctacacatgcaacacacgtgtcttacc	247	
DB 181	gctgctgcaacaactcgtgacacacgtgctcctcctacacatgcaacacacgtgtcttacc	240	
OY 248	actgctgtaagacatccagtttaccacaatgggttggagatctccgaatgtaga	307	
DB 241	actgctgtaagacatccagtttaccacaatgggttggagatctccgaatgtaga	300	
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DB 301	gtgtgtccctgagatggaalacagcttgagctctctgcaatgggttcaacacttcatgc	359	
OY 368	ttcctgtgattcattcaactacttacctgtgctcctagatatacccttattctaatcag	427	
DB 360	ttcctgtgattcattcaactacttacctgtgctcctagatatacccttattctaatcag	419	
OY 428	tttatttcttcttcaataaaaaataacatgagagagctaca	470	
DB 420	tttatttcttcttcaataaaaaataacatgagagagctaca	462	

[illegible]

OY 361 ttcatgcttcctgtgatcttccaaactactacc 397  
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Db 360 ttcatgcttcctgtgatcttccaaactactacc 396

## RESULT 10

AX240676 308 bp DNA linear PAT 26-SEP-2001  
LOCUS  
DEFINITION Sequence 2 from Patent WO0165262.  
ACCESSION AX240676  
VERSION AX240676.1 GI:15797659  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 308)  
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,  
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,  
Roberts-Rapp, L., Russell, J.C., and Stroupe, S.D.  
Reagents and methods useful for detecting diseases of the breast  
Patent: WO 0165262-A 2 07-SEP-2001.

TITLE  
JOURNAL ABBOTT LABORATORIES (US)  
FEATURES  
source 1..308 Location/Qualifiers

BASE COUNT 63 a 94 c 65 g 86 t  
ORIGIN /organism="Homo sapiens"  
/db\_xref="taxon:9606"

Query Match 63.9%; Score 300.8; DB 6; Length 308;  
Best Local Similarity 99.3%; Pred. No. 2, 2e-61;

Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctctgaagcattttgtctgtcctcctgatacttcaggtaccaccacatgaagttcttagc 60  
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Db 5 CTTTGAAGCATTTTGTCTGTCTGCTCCCTGATCTTCAGGTACCAACCTGAGTTCTTAGC 64  
OY 61 agtccgtgactccttggagattccatcttctgtctctgcccagaatccgaacaagc 120  
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Db 65 AGTCTGTGACTCTTGCGAGTTTCATCTTCTGCTCTGCCAGAACTCGAACACAGC 124  
OY 121 tgcctcagctggaacagatccaaactactgtctcctgtcgtatgagaagccctgagtctga 180  
|||||  
Db 125 TGCTCCAGCTGACAGTATCCAGTACTGTGCTCTGATGATGAGCCCTGATGCTGA 184  
OY 181 aaccactgtctgcaacaactggaacactgtctgctcctaccacatggaacacacgctgc 240  
|||||  
Db 185 AACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCTACCACTGCAACACCGCTGC 244  
OY 241 ttctaccactgtctggaagaacatctcaagtttaccacaaatgggttggagatctccgaa 300  
|||||  
Db 245 TTCTACCACTGCTGCTGAAGACATTCAGTTTACCCAAATGGGTTGGGATCTTCGGA 304  
OY 301 tggc 304  
|||||  
Db 305 TGGT 308

## RESULT 11

BD007429 308 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION Reagent and method useful in detecting mammary diseases.  
ACCESSION BD007429  
VERSION BD007429.1 GI:18635800  
KEYWORDS JP 2001503980-A/2.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 308)  
AUTHORS Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,

Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,  
Russell, J.C., and Stroupe, S.D.  
Reagent and method useful in detecting mammary diseases  
Patent: JP 2001503980-A 2 27-MAR-2001;

## COMMENT

OS Unidentified  
PN JP 2001503980-A/2  
PD 27-MAR-2001  
PF 31-OCT-1997 JP 1998520795  
PR 31-OCT-1996 US 08/742067  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACY L COLPITTS, PI  
POLA N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, PI MICHAEL  
R KLAS,  
PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI  
STEVEN D STROUPE  
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47,  
PC C07K16/30,  
PC C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00, PC  
A61K37/02  
CC Strandedness: Single;  
CC Topology: Linear;  
FH key  
FT source 1..308 Location/Qualifiers

FEATURES  
source 1..308 Location/Qualifiers  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 63 a 94 c 65 g 86 t  
ORIGIN

Query Match 63.9%; Score 300.8; DB 6; Length 308;  
Best Local Similarity 99.3%; Pred. No. 2, 2e-61;

Matches 302; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctctgaagcattttgtctgtcctcctgatacttcaggtaccaccacatgaagttcttagc 60  
|||||  
Db 5 CTTTGAAGCATTTTGTCTGTCTGCTCCCTGATCTTCAGGTACCAACCTGAGTTCTTAGC 64  
OY 61 agtccgtgactccttggagattccatcttctgtctctgcccagaatccgaacaagc 120  
|||||  
Db 65 AGTCTGTGACTCTTGCGAGTTTCATCTTCTGCTCTGCCAGAACTCGAACACAGC 124  
OY 121 tgcctcagctggaacagatccaaactactgtctcctgtcgtatgagaagccctgagtctga 180  
|||||  
Db 125 TGCTCCAGCTGACAGTATCCAGTACTGTGCTCTGATGATGAGCCCTGATGCTGA 184  
OY 181 aaccactgtctgcaacaactggaacactgtctgctcctaccacatggaacacacgctgc 240  
|||||  
Db 185 AACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCTACCACTGCAACACCGCTGC 244  
OY 241 ttctaccactgtctggaagaacatctcaagtttaccacaaatgggttggagatctccgaa 300  
|||||  
Db 245 TTCTACCACTGCTGCTGAAGACATTCAGTTTACCCAAATGGGTTGGGATCTTCGGA 304  
OY 301 tggc 304  
|||||  
Db 305 TGGT 308

## RESULT 12

AX240677 292 bp DNA linear PAT 26-SEP-2001  
LOCUS  
DEFINITION Sequence 3 from Patent WO0165262.  
ACCESSION AX240677  
VERSION AX240677.1 GI:15797660  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 292)

AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,  
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,  
Roberts-Kapp, L., Russell, J.C., and Strope, S.D.  
TITLE Reagents and methods useful for detecting diseases of the breast  
JOURNAL Patent: WO 0165262-A 3 07-SEP-2001;  
ABBOTT LABORATORIES (US)  
FEATURES location/Qualifiers  
source 1. .292  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="EST Clone 901429"

BASE COUNT 59 a 92 c 59 g 80 t 2 others  
ORIGIN

Query Match 60.9%; Score 286.8; DB 6; Length 292;  
Best Local Similarity 98.6%; Pred. No. 4.6e-58;  
Matches 288; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 gcatattgtctgtcctccatcgaagtcacacacatgaagttcttagcaagtcctg 67  
|||||  
Db 1 GCATTTTGTCTGTGCTCCCTGATCTTCATGTACACACCATGAAGTTCTTAGCAGTCTG 60  
|||||

OY 68 gtaactcttgaggatcttcacatcttctgtctctgcccagaatccgacaagctgctcca 127  
|||||  
Db 61 GTACTCTTGGGAGTTTCATCTTCTGTCTCTGCTCCAGAAATCCGACAAAGCTGCTCA 120  
|||||

OY 128 gctgaacagatccagctactgtctctgtctgaatgaagccctgtagtctgaaccact 187  
|||||  
Db 121 GCTGACAGCTATCCAGCTACTGCTGCTGATGATGAAGCCCTGATGCTGAAGAACACT 180  
|||||

OY 188 gctctcaaaaactgagacacactgctgctctctcaactgaaccacccgctgcttacc 247  
|||||  
Db 181 GCTCTGCAACCACTGGACACACTGCTGCTCTCAACATGCACACCGCTGCTTATAC 240  
|||||

OY 248 actgctcgtaaaagacatccagtttaccacaaatgggttgaggatctcccca 299  
|||||  
Db 241 ACTGCTGTAAGACATTTNAGTTTACCCAAATGGGTGGGATCTCCCA 292  
|||||

RESULT 13  
AX328499 273 bp DNA linear PAT 07-JAN-2002  
LOCUS AX328499 Sequence 2 from Patent WO0135811.  
DEFINITION AX328499  
ACCESSION AX328499  
VERSION AX328499.1 GI:18098425  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE Mack, D. and Gish, K.C.  
TITLE Novel methods of diagnosing and determining prognosis of breast  
cancer, compositions, and methods of screening for breast cancer  
modulators  
JOURNAL Patent: WO 0135811-A 2 25-MAY-2001;  
EOS Biotechnology, Inc. (US)  
FEATURES location/Qualifiers  
source 1. .273  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 58 a 85 c 59 g 71 t  
ORIGIN

Query Match 57.3%; Score 269.8; DB 6; Length 273;  
Best Local Similarity 99.3%; Pred. No. 5.1e-54;  
Matches 271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 47 atgaagttcttaacagctccggaacaccttgaggatcttcaatcttctgtctctccag 106  
|||||  
Db 1 ATGAAGTTTACAGCTGCTGACTCTTGGGAGTTTCATCTTCTGTGCTCTGCCAG 60  
|||||

OY 107 aatccgaacagctgtctcagctgagacagatatacgaactactgtctctgtatgaatga 166  
|||||  
Db 61 AATCCGACACAGCTGTCTCCAGCTGACACGATATCAGCTACTGCTCTGTGATGATCA 120  
|||||

OY 167 gccctgatgtcgaacacactgtctcgaacaaactgaagacacactgtctcttaccact 226  
|||||  
Db 121 GCCCTGATGTGAACACACTGCTGTGCAACGACTGCAACACTGCTGCTTACTACT 180  
|||||

OY 227 gcaacacacgctgtcttaccactgtctgaagacatccagtttaccacaaatggt 286  
|||||  
Db 181 GCAACACACGCTGCTTACACACTGCTGTAAAGACATTCAGTTTACCAATGAGCTT 240  
|||||

OY 287 gggatctccgaatggaagtgatgtccctga 319  
|||||  
Db 241 GGGATCTCCGAAATGATGATGATGTGCTCTCA 273  
|||||

RESULT 14  
AX079476 264 bp DNA linear PAT 22-FEB-2001  
LOCUS AX079476 Sequence 220 from Patent WO0107611.  
DEFINITION AX079476  
ACCESSION AX079476  
VERSION AX079476.1 GI:13159036  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE Baker, K.P., Goddard, A. and Wood, W. I.  
TITLE Human polypeptides and methods for the use thereof  
JOURNAL Patent: WO 0107611-A 220 01-FEB-2001;  
Genentech, Inc. (US)  
FEATURES location/Qualifiers  
source 1. .264  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 54 a 87 c 53 g 70 t  
ORIGIN

Query Match 54.3%; Score 255.6; DB 6; Length 264;  
Best Local Similarity 98.5%; Pred. No. 1.2e-50;  
Matches 258; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 cttgaagcaatttctgtctgtctcctgactcagacagacacacacgaagttcttacc 60  
|||||  
Db 3 CTTGAAGCACTTTTGTGTGCTGCTGATCTTCAGGTACCCCATGAACTTCTTAC; 62  
|||||

OY 61 agtccgtactcttggaagtttccatcttctgtctctgcccagaatccgacaacacac 120  
|||||  
Db 63 AGTCTGTACTCTTGGAGTTTCCATCTTCTGCTCTGCCCAATCCGACAAACAC 122  
|||||

OY 121 tgtctagctggaagatatacagactactgtctgctgaatgaagacccctgaatga 180  
|||||  
Db 123 TGCTCAGCTGACAGCTATTCACACTGCTGCTGATGAAGACCCCTGATGCTGA 182  
|||||

OY 181 aaccactgtctcgaacacactgagacacactgtctgtcttaccactgaacacacacac 240  
|||||  
Db 183 AACCACTGCACTGCAACACAGCTGCAACAGCTGCTGCTTACTGACTGCAACACGCT 242  
|||||

OY 241 ttctaccactgtctgtaaacac 262  
|||||  
Db 243 TTCTACCACTGCTGTAAGAC 264  
|||||

RESULT 15  
AX079475 266 bp DNA linear PAT 22-FEB-2001  
LOCUS AX079475 Sequence 219 from Patent WO0107611.  
DEFINITION AX079475  
ACCESSION AX079475  
VERSION AX079475.1 GI:13159035

KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 266)  
TITLE Baker, K.P., Goddard, A. and Wood, W.I.  
JOURNAL Human polypeptides and methods for the use thereof  
Patent: WO 0107611-A 219 01-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..266  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 54 a 88 c 54 g 70 t  
ORIGIN

Query Match 54.3%; Score 255.6; DB 6; Length 266;  
Best Local Similarity 98.5%; Pred. No. 1.2e-50;  
Matches 258; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 cttgaagcatttctgtctgtccctgaatctcaagtcacccatgaagttcttaac 60  
|||||  
Db 5 ctttgaaagcatttctgtctgtccctgaatctcaagtcacccatgaagttcttaac 64  
QY 61 agtcctgtactcttggaagttccatcttctgtctctgtccagaatccgaacaacg 120  
|||||  
Db 65 agtcctgtactcttggaagttccatcttctgtctctgtccagaatccgaacaacg 124  
QY 121 tgcctcagctgacagctalccagctactggtcctgtctgatgatlgaagccctgagtga 180  
|||||  
Db 125 tgcctcagctgacagctatccagctactggtcctgtctgatgatlgaagccctgagtga 184  
QY 181 aaccactgtcgtcgacaacactcgaccactgtgtctcctaccactgcaaccacgcgtgc 240  
|||||  
Db 185 AACCACTGCAACTGCAACCACTGCAACCACTGCTGCTCTACCACTGCAACCACTGCTGC 244  
QY 241 ttctaccactgtcgtcgaagac 262  
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Db 245 TTCTACCACGTGCTGTAAGAC 266

Search completed: October 5, 2002, 05:40:29  
Job time: 5984 sec